IN THE CLAIMS:

Claim 9 has been canceled. Please note that all claims currently pending and under consideration in the referenced application are shown below. Please enter these claims as amended. This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1-13. (Canceled)

14. (Previously Presented) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting for each data trace one or more alignment points corresponding to an internal peak associated with internal bases that are highly conserved in the target nucleic acid, and further selecting alignment points selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers, and assigning to each alignment point a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) assigning a sequence position number to each peak in each of the plurality of data traces that maximizes the number of times that the sequence position number and the reference position number are assigned to a base of the same type; and

(c) aligning the data traces based on the assigned sequence position numbers.

15. (Previously Presented) The method of claim 14, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

16. (Previously Presented) The method of claim 14, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

17. (Previously Presented) The method of claim 14, wherein four data traces, one for each nucleotide base type, are aligned.

18. (Previously Presented) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting a set of three or more alignment points for each data trace, said alignment points being selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers, and one or more internal peaks associated with internal bases that are highly conserved in the target nucleic acid, and assigning to each alignment point a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) determining the average peak spacing interval between each of the alignment points in each of the plurality of data traces and assigning sequence position numbers to peaks occurring at each interval that maximizes the number of times that the sequence position number and the reference position number are assigned to a base of the same type, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers; and

(c) aligning the data traces based on the assigned sequence position numbers.

19. (Previously Presented) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting a set of five or more alignment points for each data trace, said alignment points being selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers, and one or more internal peaks associated with internal bases that are highly conserved in the target nucleic acid, and assigning to each alignment point a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) determining the average peak spacing interval between each of the alignment points in each of the plurality of data traces and assigning sequence position numbers to peaks occurring at each interval that maximizes the number of times that the sequence position number and the reference position number are assigned to a base of the same type, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers; and

(c) aligning the data traces based on the assigned sequence position numbers.

20. (Previously Presented) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting for each data trace one or more alignment points corresponding to an internal peak associated with internal bases that are highly conserved in the target nucleic acid, and assigning to each alignment point a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) determining the average peak spacing interval between each of the alignment points in each of the plurality of data traces and assigning sequence position numbers to peaks occurring at each interval that maximizes the number of times that the sequence position number and the reference position number are assigned to a base of the same type, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers; and

(c) aligning the data traces based on the assigned sequence position numbers.

21. (Previously Presented) The method of claim 14, further comprising the steps of determining the average peak spacing interval between each of the alignment points and assigning a sequence position number to peaks occurring at each interval, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.

22. (Previously Presented) The method of claim 18, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

23. (Previously Presented) The method of claim 18, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

24. (Previously Presented) The method of claim 18, wherein four data traces, one for each nucleotide base type, are aligned.

25. (Previously Presented) The method of claim 19, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

26. (Previously Presented) The method of claim 19, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

27. (Previously Presented) The method of claim 19, wherein four data traces, one for each nucleotide base type, are aligned.

28. (Previously Presented) The method of claim 20, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

29. (Previously Presented) The method of claim 20, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

30. (Previously Presented) The method of claim 20, wherein four data traces, one for each nucleotide base type, are aligned.